RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/647,982

Source: Disc

Date Processed by STIC: 9-3-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
                http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202 .
                Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _____

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ✗ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

```
              RAW SEQUENCE LISTING              DATE: 09/03/2003
              PATENT APPLICATION:  US/10/647,982     TIME: 10:50:42

              Input Set : A:\01313.txt
              Output Set: N:\CRF4\09032003\J647982.raw

       3 <110> APPLICANT: Kaytes, Paul
       4        Teng, Chi-Hse
       6 <120> TITLE OF INVENTION: Single Nucleotide Polymorphisms Diagnostic for Schizophrenia
       8 <130> FILE REFERENCE: 01313.PRO1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/647,982
C--> 10 <141> CURRENT FILING DATE: 2003-08-26
      10 <160> NUMBER OF SEQ ID NOS: 42
      12 <170> SOFTWARE: PatentIn version 3.0
      14 <210> SEQ ID NO: 1
      15 <211> LENGTH: 3080
      16 <212> TYPE: DNA
      17 <213> ORGANISM: Homo sapiens
      19 <220> FEATURE:
      20 <221> NAME/KEY: variation
      21 <222> LOCATION: (194)..(194)
      22 <223> OTHER INFORMATION: polymorphism G or A
      25 <220> FEATURE:
      26 <221> NAME/KEY: variation
      27 <222> LOCATION: (601)..(601)
      28 <223> OTHER INFORMATION: polymorphism A or G
      31 <220> FEATURE:
      32 <221> NAME/KEY: variation
      33 <222> LOCATION: (1029)..(1029)
      34 <223> OTHER INFORMATION: polymorphism A or G
      37 <220> FEATURE:
      38 <221> NAME/KEY: variation
      39 <222> LOCATION: (1038)..(1038)
      40 <223> OTHER INFORMATION: polymorphism C or G
      43 <220> FEATURE:
      44 <221> NAME/KEY: variation
      45 <222> LOCATION: (1074)..(1074)
      46 <223> OTHER INFORMATION: polymorphism A or C
      49 <220> FEATURE:
      50 <221> NAME/KEY: variation
      51 <222> LOCATION: (2106)..(2106)
      52 <223> OTHER INFORMATION: polymorphism G or A
      55 <220> FEATURE:
      56 <221> NAME/KEY: variation
      57 <222> LOCATION: (2185)..(2185)
      58 <223> OTHER INFORMATION: polymorphism G or A
      61 <220> FEATURE:
      62 <221> NAME/KEY: variation
      63 <222> LOCATION: (2359)..(2359)
```

P. 4-5

Does Not Comply
Corrected Diskette Needed

```
 64 <223> OTHER INFORMATION: polymorphism T or G
 67 <220> FEATURE:
 68 <221> NAME/KEY: variation
 69 <222> LOCATION: (2663)..(2663)
 70 <223> OTHER INFORMATION: polymorphism C or G
 73 <220> FEATURE:
 74 <221> NAME/KEY: variation
 75 <222> LOCATION: (2796)..(2796)
 76 <223> OTHER INFORMATION: polymorphism A or G
 79 <400> SEQUENCE: 1
 80 agtaggaatc agatagcgag attgattaat aataatactt atcactcttt ataacttgaa    60
 82 aagcaagttc acaaatgtct ctaaagtcac agccctgtac tggaaagaga gttgaaccct   120
 84 tcttcaggaa gacaataata taataataac aatattttct tcactctgca gtgtctttac   180
W--> 86 attccagggt tggnaacatt actgaggatt ctcttcccat tttccagttt cctgttcatt   240
 88 attcttattt ttttgactgc ttttagcatc gggagcacaa aggccagtca ccaggaattg   300
 90 caaacaaatg cgtagtcaga gagagagggc tcactgccca tttgtcatgt ggatgcagac   360
 92 acattgcaga tgtgttccca gtaacaatgt cttgagaaga ggactggtct ttccaccagc   420
 94 atctcagaaa tgccggtgtg tctaaacagc atgtcgttct ttaatgcttt catgcaatat   480
 96 attttatcaa tctcaagttc ccctcactat gtattataat aatttctgct tgttggtaac   540
 98 caatgcagat ggaaaattga ttcttaacag aagagaaaga gccaagtatt gatgcttact   600
100 ntttacaccc tattgtatct ttgtaacaaa aacccgggtg gctaagttat gattgggaac   660
102 aagggaatgg ttcaagtcta tgcactaagg aaaaacaaat ctttggccta aaacaataat   720
104 gataatagaa tttaatatag agtagagacc tgttttgtag aataactttc ctagtaatca   780
106 ctgttgaaaa taatcatact agttcacacc gcgcactaca gggattccat cgagggattt   840
108 tcccattgaa ggcatttatt tagctaaaag gacttcatct ttaaggcggt aatgcaggac   900
110 agataacaga gataaagata acaggaggtg atctttcagc tccataatta cattccatat   960
112 cagcgactgt tgcacagaga aactcaaaag gtaaaaataa aatatgaaag gatatttaaa  1020
114 atcaaaagna attttatnaa attaagagca tgagacattt atcagttgaa acantctcca  1080
116 ataatcttgt gcaatataat ttttgtcaaa ttttattttg tcataaacat ttgggattta  1140
118 taataaaaat ggaaacttga aaaattatat tagagataat atctgatcat ttcctctggc  1200
120 atcctggtga atatgtgttt ttttccgcag gagcactgaa aatcaggaac aatcctgtat  1260
122 tttttgtgat aatcaacaag gacaaaactt ctccatatgt aaataacagc gttatgagca  1320
124 gcaattcatc cctgctggtg gctgtgcagc tgtgctacgc gaacgtgaat gggtcctgtg  1380
126 tgaaaatccc cttctcgccg ggatcccggg tgattctgta catagtgttt ggctttgggg  1440
128 ctgtgctggc tgtgtttgga aacctcctgg tgatgatttc aatcctccat ttcaagcagc  1500
130 tgcactctcc gaccaatttt ctcgttgcct ctctggcctg cgctgatttc ttggtgggtg  1560
132 tgactgtgat gcccttcagc atggtcagga cggtggagag ctgctggtat tttgggagga  1620
134 gttttgtac tttccacacc tgctgtgatg tggcattttg ttactcttct ctctttcact  1680
136 tgtgcttcat ctccatcgac aggtacattg cggttactga cccccctggtc tatcctacca  1740
138 agttcaccgt atctgtgtca ggaatttgca tcagcgtgtc ctggatcctg cccctcatgt  1800
140 acagcggtgc tgtgttctac acaggtgtct atgacgatgg gctggaggaa ttatctgatg  1860
142 ccctaaactg tataggaggt tgtcagaccg ttgtaaatca aaactgggtg ttgacagatt  1920
144 ttctatcctt ctttatacct acctttatta tgataattct gtatggtaac atatttcttg  1980
146 tggctagacg acaggcgaaa aagatagaaa atactggtag caagacagaa tcatcctcag  2040
148 agagttacaa agccagagtg gccaggagag agagaaaagc agctaaaacc ctgggggtca  2100
150 cagtgntagc atttatgatt tcatggttac catatagcat tgattcatta attgatgcct  2160
152 ttatgggctt tataacccct gcctntattt atgagatttg ctgttggtgt gcttattata  2220
154 actcagccat gaatcctttg atttatgctt tattttaccc atggtttagg aaagcaataa  2280
156 aagttattgt aactggtcag gttttaaaga acagttcagc aaccatgaat ttgttttctg  2340
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158 aacatatata agcagttgna tagacgaagt tcaggatacc tttaaaatta ccaagcgaaa  2400
160 tgagttttta aaaatcaagt aagactatga atgaatagca aataaattgc tcttcaaatg  2460
162 aaaaacaaat caatgttttt cagtcttgtt aagatgtgca ctttcctgtc ccttctgcaa  2520
164 aagtatttac ttggctaaca aatgttaaat tcctatttgt taactgcttt agagctcagc  2580
166 atatcccact ccctgcagac acttttttgtc ttttaatcca ttgactcttc cctctgctct  2640
168 ggtattttc ctaaaaatat ttntgttttt ttttttttta tttattccct ttcctctttt  2700
170 ctttacaaag ctttctactc tttcccagcc tgccaaaaat ttcatttgtg aatagccttt  2760
172 atcaaattat tggtttcttt tgctttggtt attttnccac aggagtcctt ttaggtatta  2820
174 atttaattta ttcaatcttg ggagagatct cagggtgtat ggggcaattt gcaaatgaag  2880
176 acatcatctt gaccaggctg ttgtaattgt caaaccagtt actgtcattc ttgtaattat  2940
178 ttcctccccc aaagtgggaa gcagaagcca ctgtacttcc cagaatgatg ttaggatgat  3000
180 tatttggctg ctgttcttgc tattgcacaa aactgtttaa agagttggta tgaatagagc  3060
182 cctgtgttac attattcagt                                              3080
185 <210> SEQ ID NO: 2
186 <211> LENGTH: 345
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
190 <220> FEATURE:
191 <221> NAME/KEY: VARIANT
192 <222> LOCATION: (265)..(265)
193 <223> OTHER INFORMATION: Polymorphic Amino Acid Val or Ile
196 <220> FEATURE:
197 <221> NAME/KEY: VARIANT
198 <222> LOCATION: (291)..(291)
199 <223> OTHER INFORMATION: Polymorphic Amino Acid Cys or Tyr
202 <400> SEQUENCE: 2
204 Met Ser Ser Asn Ser Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala
205 1               5                   10                  15
207 Asn Val Asn Gly Ser Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg
208             20                  25                  30
210 Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe
211         35                  40                  45
213 Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His
214     50                  55                  60
216 Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala Cys Ala Asp Phe Leu
217 65                  70                  75                  80
219 Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser
220             85                  90                  95
222 Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp
223             100                 105                 110
225 Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile
226         115                 120                 125
228 Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe
229     130                 135                 140
231 Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro
232 145                 150                 155                 160
234 Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Tyr Asp Asp Gly
235                 165                 170                 175
237 Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile Gly Gly Cys Gln Thr
```

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238               180                    185                    190
240 Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe Leu Ser Phe Phe Ile
241               195                    200                    205
243 Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn Ile Phe Leu Val Ala
244               210                    215                    220
246 Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Gly Ser Lys Thr Glu Ser
247 225                    230                    235                    240
249 Ser Ser Glu Ser Tyr Lys Ala Arg Val Ala Arg Arg Glu Arg Lys Ala
250               245                    250                    255
W--> 252 Ala Lys Thr Leu Gly Val Thr Val Xaa Ala Phe Met Ile Ser Trp Leu
253               260                    265                    270
255 Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly Phe Ile Thr
256               275                    280                    285
258 Pro Ala Xaa Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr Tyr Asn Ser
259               290                    295                    300
261 Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys
262 305                    310                    315                    320
264 Ala Ile Lys Val Ile Val Thr Gly Gln Val Leu Lys Asn Ser Ser Ala
265               325                    330                    335
267 Thr Met Asn Leu Phe Ser Glu His Ile
268               340                    345
270 <210> SEQ ID NO: 3
271 <211> LENGTH: 24
272 <212> TYPE: DNA
273 <213> ORGANISM: synthetic construct
275 <400> SEQUENCE: 3
276 agtaggaatc agatagcgag attg                                          24
279 <210> SEQ ID NO: 4
280 <211> LENGTH: 24
281 <212> TYPE: DNA
282 <213> ORGANISM: synthetic construct
284 <400> SEQUENCE: 4
285 actgaataat gtaacacagg gctc                                          24
288 <210> SEQ ID NO: 5
289 <211> LENGTH: 20
290 <212> TYPE: DNA
291 <213> ORGANISM: synthetic construct
293 <400> SEQUENCE: 5
294 tgcgtagtca gagagagagg                                               20
297 <210> SEQ ID NO: 6
298 <211> LENGTH: 21
299 <212> TYPE: DNA
300 <213> ORGANISM: synthetic construct
302 <400> SEQUENCE: 6
303 agccagcaca gccccaaagc c                                             21
306 <210> SEQ ID NO: 7
307 <211> LENGTH: 21
308 <212> TYPE: DNA
309 <213> ORGANISM: synthetic construct
```

1) See item 10 on error summary sheet.

RAW SEQUENCE LISTING   DATE: 09/03/2003
PATENT APPLICATION: **US/10/647,982**   TIME: 10:50:42

Input Set : **A:\01313.txt**
Output Set: **N:\CRF4\09032003\J647982.raw**

```
311 <400> SEQUENCE: 7
312 tctatgacga tgggctggag g                                         21
315 <210> SEQ ID NO: 8
316 <211> LENGTH: 21
317 <212> TYPE: DNA
318 <213> ORGANISM: synthetic construct
320 <400> SEQUENCE: 8
321 atagacgaag ttcaggatac c                                         21
324 <210> SEQ ID NO: 9
325 <211> LENGTH: 15
326 <212> TYPE: DNA
327 <213> ORGANISM: synthetic construct
329 <400> SEQUENCE: 9
330 cagggttggg aacat                                                15
333 <210> SEQ ID NO: 10
334 <211> LENGTH: 16
335 <212> TYPE: DNA
336 <213> ORGANISM: synthetic construct
338 <400> SEQUENCE: 10
339 agggttggaa acatta                                               16
342 <210> SEQ ID NO: 11
343 <211> LENGTH: 20
344 <212> TYPE: DNA
345 <213> ORGANISM: synthetic construct
347 <400> SEQUENCE: 11
348 atccttacta tttcaccct                                            20
351 <210> SEQ ID NO: 12
352 <211> LENGTH: 18
353 <212> TYPE: DNA
354 <213> ORGANISM: synthetic construct
356 <400> SEQUENCE: 12
357 atgcttactg tttacacc                                             18
360 <210> SEQ ID NO: 13
361 <211> LENGTH: 19
362 <212> TYPE: DNA
363 <213> ORGANISM: synthetic construct
365 <400> SEQUENCE: 13
366 tgctcttaat ttgataaaa                                            19
369 <210> SEQ ID NO: 14
370 <211> LENGTH: 19
371 <212> TYPE: DNA
372 <213> ORGANISM: synthetic construct
374 <400> SEQUENCE: 14
375 tgctcttaat ttcataaaa                                            19
378 <210> SEQ ID NO: 15
379 <211> LENGTH: 20
380 <212> TYPE: DNA
381 <213> ORGANISM: synthetic construct
383 <400> SEQUENCE: 15
```

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/03/2003
PATENT APPLICATION: **US/10/647,982**   TIME: 10:50:43

Input Set : **A:\01313.txt**
Output Set: **N:\CRF4\09032003\J647982.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 194,601,1029,1038,1074,2106,2185,2359,2663,2796
Seq#:2; Xaa Pos. 265,291

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/647,982**

DATE: 09/03/2003
TIME: 10:50:43

Input Set : **A:\01313.txt**
Output Set: **N:\CRF4\09032003\J647982.raw**

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:180
M:341 Repeated in SeqNo=1
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:256
M:341 Repeated in SeqNo=2
```